Gang G Wang

List of Publications by Year
in descending order

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70 papers	8,206 citations	71102 41 h-index	95266 68 g-index
72 all docs	72 docs citations	72 times ranked	11957 citing authors

#	Article	IF	Citations
1	A NSD3-targeted PROTAC suppresses NSD3 and cMyc oncogenic nodes in cancer cells. Cell Chemical Biology, 2022, 29, 386-397.e9.	5.2	30
2	Reprogramming CBX8-PRC1 function with a positive allosteric modulator. Cell Chemical Biology, 2022, 29, 555-571.e11.	5.2	12
3	Cell type-specific chromatin topology and gene regulation. Trends in Genetics, 2022, 38, 413-415.	6.7	1
4	DOT1L activity in leukemia cells requires interaction with ubiquitylated H2B that promotes productive nucleosome binding. Cell Reports, 2022, 38, 110369.	6.4	11
5	EZH2 noncanonically binds cMyc and p300 through a cryptic transactivation domain to mediate gene activation and promote oncogenesis. Nature Cell Biology, 2022, 24, 384-399.	10.3	88
6	A PRC2-Kdm5b axis sustains tumorigenicity of acute myeloid leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	11
7	Oncogenic fusion proteins and their role in three-dimensional chromatin structure, phase separation, and cancer. Current Opinion in Genetics and Development, 2022, 74, 101901.	3.3	11
8	Discovery of a dual WDR5 and Ikaros PROTAC degrader as an anti-cancer therapeutic. Oncogene, 2022, 41, 3328-3340.	5.9	18
9	DNMT3A mutations define a unique biological and prognostic subgroup associated with cytotoxic T cells in PTCL-NOS. Blood, 2022, 140, 1278-1290.	1.4	20
10	ZMYND11-MBTD1 induces leukemogenesis through hijacking NuA4/TIP60 acetyltransferase complex and a PWWP-mediated chromatin association mechanism. Nature Communications, 2021, 12, 1045.	12.8	27
11	Cistrome analysis of YY1 uncovers a regulatory axis of YY1:BRD2/4-PFKP during tumorigenesis of advanced prostate cancer. Nucleic Acids Research, 2021, 49, 4971-4988.	14.5	22
12	A conserved BAH module within mammalian BAHD1 connects H3K27me3 to Polycomb gene silencing. Nucleic Acids Research, 2021, 49, 4441-4455.	14.5	15
13	The language of chromatin modification in human cancers. Nature Reviews Cancer, 2021, 21, 413-430.	28.4	179
14	DNMT1 reads heterochromatic H4K20me3 to reinforce LINE-1 DNA methylation. Nature Communications, 2021, 12, 2490.	12.8	63
15	Phase separation drives aberrant chromatin looping and cancer development. Nature, 2021, 595, 591-595.	27.8	197
16	Polycomb Gene Silencing Mechanisms: PRC2 Chromatin Targeting, H3K27me3 'Readout', and Phase Separation-Based Compaction. Trends in Genetics, 2021, 37, 547-565.	6.7	71
17	Harnessing the E3 Ligase KEAP1 for Targeted Protein Degradation. Journal of the American Chemical Society, 2021, 143, 15073-15083.	13.7	66
18	A selective WDR5 degrader inhibits acute myeloid leukemia in patient-derived mouse models. Science Translational Medicine, 2021, 13, eabj1578.	12.4	67

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19	R-loop and its functions at the regulatory interfaces between transcription and (epi)genome. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2021, 1864, 194750.	1.9	15
20	Direct readout of heterochromatic H3K9me3 regulates DNMT1-mediated maintenance DNA methylation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 18439-18447.	7.1	62
21	BAHCC1 binds H3K27me3 via a conserved BAH module to mediate gene silencing and oncogenesis. Nature Genetics, 2020, 52, 1384-1396.	21.4	57
22	No Easy Way Out for EZH2: Its Pleiotropic, Noncanonical Effects on Gene Regulation and Cellular Function. International Journal of Molecular Sciences, 2020, 21, 9501.	4.1	45
23	E2A-PBX1 functions as a coactivator for RUNX1 in acute lymphoblastic leukemia. Blood, 2020, 136, 11-23.	1.4	33
24	Mechanistic insights into chromatin targeting by leukemic NUP98-PHF23 fusion. Nature Communications, 2020, 11, 3339.	12.8	15
25	Comprehensive structure-function characterization of DNMT3B and DNMT3A reveals distinctive de novo DNA methylation mechanisms. Nature Communications, 2020, 11, 3355.	12.8	94
26	Epigenetic Control of Cdkn2a.Arf Protects Tumor-Infiltrating Lymphocytes from Metabolic Exhaustion. Cancer Research, 2020, 80, 4707-4719.	0.9	19
27	PHF19 promotes multiple myeloma tumorigenicity through PRC2 activation and broad H3K27me3 domain formation. Blood, 2019, 134, 1176-1189.	1.4	57
28	R-loops: formation, function, and relevance to cell stress. Cell Stress, 2019, 3, 38-46.	3.2	81
29	Structure and regulation of ZCCHC4 in m6A-methylation of 28S rRNA. Nature Communications, 2019, 10, 5042.	12.8	72
30	Discovery and Characterization of a Cellular Potent Positive Allosteric Modulator of the Polycomb Repressive Complex 1 Chromodomain, CBX7. Cell Chemical Biology, 2019, 26, 1365-1379.e22.	5.2	38
31	Understanding histone H3 lysine 36 methylation and its deregulation in disease. Cellular and Molecular Life Sciences, 2019, 76, 2899-2916.	5.4	100
32	A Model System for Studying the DNMT3A Hotspot Mutation (DNMT3AR882) Demonstrates a Causal Relationship between Its Dominant-Negative Effect and Leukemogenesis. Cancer Research, 2019, 79, 3583-3594.	0.9	18
33	BCL2 Amplicon Loss and Transcriptional Remodeling Drives ABT-199 Resistance in B Cell Lymphoma Models. Cancer Cell, 2019, 35, 752-766.e9.	16.8	56
34	Interaction between androgen receptor and coregulator SLIRP is regulated by Ack1 tyrosine kinase and androgen. Scientific Reports, 2019, 9, 18637.	3.3	7
35	The Chromatin Remodeler BPTF Activates a Stemness Gene-Expression Program Essential for the Maintenance of Adult Hematopoietic Stem Cells. Stem Cell Reports, 2018, 10, 675-683.	4.8	26
36	Structural basis for DNMT3A-mediated de novo DNA methylation. Nature, 2018, 554, 387-391.	27.8	215

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37	ZFX Mediates Non-canonical Oncogenic Functions of the Androgen Receptor Splice Variant 7 in Castrate-Resistant Prostate Cancer. Molecular Cell, 2018, 72, 341-354.e6.	9.7	64
38	Pharmacologic Targeting of Chromatin Modulators As Therapeutics of Acute Myeloid Leukemia. Frontiers in Oncology, 2017, 7, 241.	2.8	21
39	Bmi1 Is a Key Epigenetic Barrier to Direct Cardiac Reprogramming. Cell Stem Cell, 2016, 18, 382-395.	11.1	186
40	BPTF Is Essential for T Cell Homeostasis and Function. Journal of Immunology, 2016, 197, 4325-4333.	0.8	31
41	Epigenetic Perturbations by Arg882-Mutated DNMT3A Potentiate Aberrant Stem Cell Gene-Expression Program and Acute Leukemia Development. Cancer Cell, 2016, 30, 92-107.	16.8	130
42	PBX3 and MEIS1 Cooperate in Hematopoietic Cells to Drive Acute Myeloid Leukemias Characterized by a Core Transcriptome of the MLL-Rearranged Disease. Cancer Research, 2016, 76, 619-629.	0.9	45
43	Gene enhancer deregulation and epigenetic vulnerability. Oncoscience, 2016, 3, 299-301.	2.2	0
44	Selective inhibition of EZH2 and EZH1 enzymatic activity by a small molecule suppresses MLL-rearranged leukemia. Blood, 2015, 125, 346-357.	1.4	188
45	Polycomb genes, miRNA, and their deregulation in B-cell malignancies. Blood, 2015, 125, 1217-1225.	1.4	37
46	Targeting EZH2 and PRC2 dependence as novel anticancer therapy. Experimental Hematology, 2015, 43, 698-712.	0.4	101
47	An Allosteric Interaction Links USP7 to Deubiquitination and Chromatin Targeting of UHRF1. Cell Reports, 2015, 12, 1400-1406.	6.4	78
48	Histone modifications change with age, dietary restriction and rapamycin treatment in mouse brain. Oncotarget, 2015, 6, 15882-15890.	1.8	61
49	NUP98â€“PHF23 Is a Chromatin-Modifying Oncoprotein That Causes a Wide Array of Leukemias Sensitive to Inhibition of PHD Histone Reader Function. Cancer Discovery, 2014, 4, 564-577.	9.4	66
50	Tudor: a versatile family of histone methylation â€˜readersâ€™. Trends in Biochemical Sciences, 2013, 38, 546-555.	7.5	145
51	An H3K36 Methylation-Engaging Tudor Motif of Polycomb-like Proteins Mediates PRC2 Complex Targeting. Molecular Cell, 2013, 49, 571-582.	9.7	221
52	An Orally Bioavailable Chemical Probe of the Lysine Methyltransferases EZH2 and EZH1. ACS Chemical Biology, 2013, 8, 1324-1334.	3.4	399
53	Sequence Requirements for Combinatorial Recognition of Histone H3 by the MRG15 and Pf1 Subunits of the Rpd3S/Sin3S Corepressor Complex. Journal of Molecular Biology, 2012, 422, 519-531.	4.2	28
54	Covalent histone modifications â€” miswritten, misinterpreted and mis-erased in human cancers. Nature Reviews Cancer, 2010, 10, 457-469.	28.4	982

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55	Lens epithelium-derived growth factor fusion proteins redirect HIV-1 DNA integration. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3135-3140.	7.1	129
56	Multiple Interactions Recruit MLL1 and MLL1 Fusion Proteins to the HOXA9 Locus in Leukemogenesis. Molecular Cell, 2010, 38, 853-863.	9.7	186
57	Pro Isomerization in MLL1 PHD3-Bromo Cassette Connects H3K4me Readout to CyP33 and HDAC-Mediated Repression. Cell, 2010, 141, 1183-1194.	28.9	176
58	Haematopoietic malignancies caused by dysregulation of a chromatin-binding PHD finger. Nature, 2009, 459, 847-851.	27.8	392
59	"Misinterpretation" of a histone mark is linked to aberrant stem cells and cancer development. Cell Cycle, 2009, 8, 1982-3.	2.6	8
60	PHD fingers in human diseases: Disorders arising from misinterpreting epigenetic marks. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2008, 647, 3-12.	1.0	187
61	Chromatin remodeling and cancer, part I: covalent histone modifications. Trends in Molecular Medicine, 2007, 13, 363-372.	6.7	369
62	Chromatin remodeling and cancer, part II: ATP-dependent chromatin remodeling. Trends in Molecular Medicine, 2007, 13, 373-380.	6.7	202
63	Survival signaling in HoxA9/Meis1 AML. Blood, 2007, 109, 3619-3620.	1.4	1
64	NUP98â€“NSD1 links H3K36 methylation to Hox-A gene activation and leukaemogenesis. Nature Cell Biology, 2007, 9, 804-812.	10.3	395
65	Persistent Transactivation by Meis1 Replaces Hox Function in Myeloid Leukemogenesis Models: Evidence for Co-Occupancy of Meis1-Pbx and Hox-Pbx Complexes on Promoters of Leukemia-Associated Genes. Molecular and Cellular Biology, 2006, 26, 3902-3916.	2.3	86
66	Quantitative production of macrophages or neutrophils ex vivo using conditional Hoxb8. Nature Methods, 2006, 3, 287-293.	19.0	337
67	Specificity in Toll-like receptor signalling through distinct effector functions of TRAF3 and TRAF6. Nature, 2006, 439, 204-207.	27.8	836
68	Meis1 programs transcription of FLT3 and cancer stem cell character, using a mechanism that requires interaction with Pbx and a novel function of the Meis1 C-terminus. Blood, 2005, 106, 254-264.	1.4	104
69	Allelic loss and gain, but not genomic instability, as the major somatic mutation in primary hepatocellular carcinoma. Genes Chromosomes and Cancer, 2001, 31, 221-227.	2.8	64
70	Genetic aberration in primary hepatocellular carcinoma: correlation between p53 gene mutation and loss-of-hetero- zygosity on chromosome 16q21-q23 and 9p21-p23. Cell Research, 2000, 10, 311-323.	12.0	32